

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Su, Jeffrey
Rosen, Craig A.
- (ii) TITLE OF INVENTION: Death Domain Containing Receptor 5
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Human Genome Sciences, Inc.
 - (B) STREET: 9410 Key West Avenue
 - (C) CITY: Rockville
 - (D) STATE: MD
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US herewith
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/054,021
 - (B) FILING DATE: 29-JUL-1997
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/040,846
 - (B) FILING DATE: 17-MAR-1997
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hoover, Kenley
 - (B) REGISTRATION NUMBER: 40,302
 - (C) REFERENCE/DOCKET NUMBER: PF366
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 3013098504
 - (B) TELEFAX: 3013098439

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..283

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 130..1362

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 284..1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGCGTCCG CGGGCGCGGC CGGAGAACCC CGCAATCTTT GCGCCCACAA AATACACCGA	60
CGATGCCCCGA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC	120
CCTACCGCC ATG GAA CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG	168
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly	
-51 -50 -45 -40	
GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC AGG	216
Ala Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg	
-35 -30 -25	
CCT GGG CCC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC	264
Pro Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val	
-20 -15 -10	
CTG CTG TTG GTC TCA GCT GAG TCT GCT CTG ATC ACC CAA CAA GAC CTA	312
Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu	
-5 1 5 10	
GCT CCC CAG CAG AGA GCG GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA	360
Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser	
15 20 25	
GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT	408
Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp	
30 35 40	
TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TGG AAT GAC	456
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp	
45 50 55	

CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA GGT GAA GTG GAG Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu 60 65 70	504
CTA AGT CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu 75 80 85 90	552
GGC ACC TTC CGG GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg 95 100 105	600
ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA CCC TGG Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp 110 115 120	648
AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA GGA GTC Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val 125 130 135	696
ACA GTT GCA GCC GTA GTC TTG ATT GTG GCT GTG TTT GTT TGC AAG TCT Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser 140 145 150	744
TTA CTG TGG AAG AAA GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly 155 160 165 170	792
GGT GGT GGG GAC CCT GAG CGT GTG-GAC AGA AGC TCA CAA CGA CCT GGG Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly 175 180 185	840
GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC TTG CAG CCC ACC Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr 190 195 200	888
CAG GTC CCT GAG CAG GAA ATG GAA GTC CAG GAG CCA GCA GAG CCA ACA Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr 205 210 215	936
GGT GTC AAC ATG TTG TCC CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro 220 225 230	984
GCA GAA GCT GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn 235 240 245 250	1032
GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT GAC TTT GCA Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala 255 260 265	1080
GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG CTC ATG AGG AAG TTG GGC Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly 270 275 280	1128

CTC ATG GAC AAT GAG ATA AAG GTG GCT AAA GCT GAG GCA GCG GGC CAC Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His 285 290 295	1176
AGG GAC ACC TTG TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly 300 305 310	1224
CGA GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG CTG GGA Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly 315 320 325 330	1272
GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC TTG TTG AGC TCT GGA Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly 335 340 345	1320
AAG TTC ATG TAT CTA GAA GGT AAT GCA GAC TCT GCC ATG TCC Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser 350 355 360	1362
TAAGTGTGAT TCTCTTCAGG AAGTGAGACC TTCCCTGGTT TACCTTTTTT CTGGAAAAAG	1422
CCCAACTGGA CTCCAGTCAG TAGGAAAGTG CCACAATTGT CACATGACCG GTACTGGAAG	1482
AAACTCTCCC ATCCAACATC ACCCAGTGGA TGGAACATCC TGTAACTTTT CACTGCACTT	1542
GGCATTATTT TTATAAGCTG AATGTGATAA TAAGGACACT ATGGAAAAAA AAAAAAA	1600

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys -51 -50 -45 -40
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro -35 -30 -25 -20
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu -15 -10 -5
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln 1 5 10
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu 15 20 25

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 30 35 40 45
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 50 55 60
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 65 70 75
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 80 85 90
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 95 100 105
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 110 115 120 125
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 130 135 140
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 145 150 155
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
 160 165 170
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 175 180 185
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 190 195 200 205
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 210 215 220
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 225 230 235
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 240 245 250
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
 255 260 265
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
 270 275 280 285
 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
 290 295 300
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
 305 310 315

Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
 320 325 330

Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
 335 340 345

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
 350 355 360

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu

165	170	175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr		
180	185	190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser		
195	200	205
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu		
210	215	220
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys		
225	230	240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu		
245	250	255
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser		
260	265	270
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val		
275	280	285
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys		
290	295	300
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly		
305	310	315
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn		
325	330	335
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp		
340	345	350
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro		
355	360	365
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu		
370	375	380
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln		
385	390	395
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala		
405	410	415
Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly		
420	425	430
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro		
435	440	445
Pro Ala Pro Ser Leu Leu Arg		
450	455	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1           5           10 -           15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20           25           30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35           40           45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50           55           60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65           70           75           80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85           90           95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100          105          110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115          120          125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130          135          140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145          150          155          160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165          170          175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180          185          190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195          200          205

```


Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
 210 215 220
 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
 225 230 235 240
 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
 245 250 255
 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
 260 265 270
 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
 275 280 285
 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
 290 295 300
 Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
 305 310 315 320
 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
 325 330 335

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
 1 5 10 15
 Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
 20 25 30
 Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
 35 40 45
 Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
 50 55 60
 Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 65 70 75 80
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp

85					90					95						
Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	
100					105					110						
Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	
115					120					125						
Gln	Cys	Val	Ser	Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	
130					135					140						
Gly	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	
145					150					155					160	
Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	
165					170					175						
Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	
180					185					190						
Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	
195					200					205						
Gly	Leu	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	
210					215					220						
Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	
225					230					235					240	
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	
245					250					255						
Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	
260					265					270						
Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	
275					280					285						
Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	Gln	Leu	Pro	
290					295					300						
Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr	Leu	Ser	Pro	Glu	Ser	
305					310					315					320	
Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	
325					330					335						
Asp	Val	Met	Asp	Ala	Val	Pro	Ala	Arg	Arg	Trp	Lys	Glu	Phe	Val	Arg	
340					345					350						
Thr	Leu	Gly	Leu	Arg	Glu	Ala	Glu	Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	
355					360					365						
Gly	Arg	Phe	Arg	Asp	Gln	Gln	Tyr	Glu	Met	Leu	Lys	Arg	Trp	Arg	Gln	
370					375					380						

Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
 385 390 395 400

Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
 405 410 415

Pro

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT TCTGGAAAAA	60
GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA	120
AGAAACTCTC CCATCCAACA TCACCCAGTG GNATGGGAAC ACTGATGAAC TTTTCACTGC	180
ACTTGGCATT ATTTTTGTNA AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG	240
ATCATTCCGG TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG	300
CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG GTNAACATTG	360
GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCAGCT TANAATNGNN GAANANGATG	420
NATNANGAAC CTTTTTTTGG GTGGGGGGGT NNCGGGGCAG TNNAANGNNG NCTCCCCAGG	480
TTTGNGGTNG CAATNGNGGA ANNNTGG	507

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC ATTTACATTA 60
 GGATAAAAAA GTGCTGTGAA AACAAATGACA TCCCAAACCA AATCTCAAAG TACGCACAAA 120
 CGGAATGATC CAGACATTTT CATAGGTCCT TATTATCACA TTCAGCTTAT AAAATAATGC 180
 CAAGTGCAGT GAAAAGTTAC AGGATGTTCC ATCCACTGGG TGGATT 226

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCCCATGGA GTCTGCTCTG ATCAC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCAAGCTTT TAGCCTGATT CTTTGTGGAC 30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA ACAACGGGGA CAGAAC

36

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGTACCT TAGGACATGG CAGAGTC

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGTACCT TAGCCTGATT CTTTGTGGAC

30